

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 4, 2003, 16:35:42 ; Search time 1467 Seconds
(without alignments)
2142.538 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616

Sequence: 1 MAAAMDVDTPSGTNSGAGKK.....KTRQVCPLDNREWEFQKYGH 108

Scoring table: BLOSUM62

Xgapop	10.0	, Xgapext	0.5
Ygapop	10.0	, Ygapext	0.5
Fgapop	6.0	, Fgapext	7.0
Delop	6.0	, Delext	7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% .

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cggn2_1/USPTO_spool/US09541462/runat_31032003_090927_7154/app_query.fasta_1.26
3
-DB=GenEmbl -QFMT=fastap -SUFFIX=std.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09541462 @CGN_1_1_3745 _@runat_31032003_090927_7154 -NCPU=6 -ICPU=3
-NO_XLPXN -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	
	1	616	100.0	327	9	AF142059 Homo sapi
	2	616	100.0	504	10	AF140599 Mus muscu
	3	616	100.0	508	9	AF140598 Homo sapi
	4	616	100.0	544	9	BC001466 Homo sapi
	5	616	100.0	554	9	BC017370 Homo sapi
	6	616	100.0	1616	10	BC027396 Mus muscu
	7	604	98.1	1933	5	AY027936 Salmo sal
	8	584	94.8	497	9	AF085906 Homo sapi
c	9	573	93.0	5347	6	AX281690 Sequence
c	10	554	89.9	3484	9	X73608 H.sapiens m
	11	545	88.5	306	9	AY099360 Homo sapi
	12	535	86.9	1181	3	AY119265 Drosophil
	13	515.5	83.7	635	8	AY086913 Arabidops
	14	515.5	83.7	666	8	AY072430 Arabidops
	15	514.5	83.5	357	8	AY052401 Arabidops
	16	514.5	83.5	544	8	AY114719 Arabidops

17	501.5	81.4	3208	6	AX212267	AX212267 Sequence
18	492.5	80.0	361	3	AB077287	AB077287 Caenorhab
19	469	76.1	324	8	AF179228	AF179228 Schizosac
20	464.5	75.4	46630	3	DMC115C2	AL031581 Drosophil
c 21	464.5	75.4	102227	2	AC020129	AC020129 Drosophil
22	464.5	75.4	161668	3	AC104602	AC104602 Drosophil
23	464.5	75.4	299970	3	AE003418	AE003418 Drosophil
c 24	433	70.3	433	11	G27926	G27926 human STS S
25	428	69.5	40197	3	CBRG33P21	AC084553 Caenorhab
26	425.5	69.1	171237	2	AC123343	AC123343 Rattus no
27	411.5	66.8	40387	8	SPAC23H4	Z98977 S.pombe chr
28	410.5	66.6	104787	9	AC109638	AC109638 Homo sapi
c 29	402.5	65.3	39874	3	CEZK287	Z70757 Caenorhabdi
30	400.5	65.0	553	3	AY070810	AY070810 Drosophil
31	400.5	65.0	750	3	AF218290	AF218290 Drosophil
c 32	400.5	65.0	3185	3	AY061302	AY061302 Drosophil
33	400.5	65.0	95294	2	AC019742	AC019742 Drosophil
34	400.5	65.0	167977	3	AC010010	AC010010 Drosophil
35	400.5	65.0	310120	3	AE003468	AE003468 Drosophil
36	385	62.5	1255	8	SCYOL134C	Z74876 S.cerevisia
37	385	62.5	12805	8	SC128XV	X95465 S.cerevisia
c 38	378	61.4	164399	3	PFMAL3P6	Z98551 Plasmodium
39	352.5	57.2	173346	9	AC112184	AC112184 Homo sapi
40	352.5	57.2	175561	9	AC012636	AC012636 Homo sapi
c 41	335.5	54.5	79677	8	ATT21C14	AL138639 Arabidops
c 42	327.5	53.2	177444	2	AC024617	AC024617 Homo sapi
43	314	51.0	209982	3	CNS06C8G	AL391737 chromosom
44	292	47.4	342	9	AF142060	AF142060 Homo sapi
c 45	292	47.4	418	6	AX332170	AX332170 Sequence

ALIGNMENTS

RESULT 1
AF142059

LOCUS AF142059 327 bp mRNA linear PRI 14-JUL-1999
DEFINITION Homo sapiens RING finger protein (ROC1) mRNA, complete cds.
ACCESSION AF142059
VERSION AF142059.1 GI:4809215
KEYWORDS .
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 327)
AUTHORS Ohta,T., Michel,J.J., Schottelius,A.J. and Xiong,Y.
TITLE ROC1, a homolog of APC11, represents a family of cullin partners
with an associated ubiquitin ligase activity
JOURNAL Mol. Cell 3 (4), 535-541 (1999)
MEDLINE 99247022
PUBMED 10230407
REFERENCE 2 (bases 1 to 327)
AUTHORS Ohta,T., Michel,J. and Xiong,Y.
TITLE Direct Submission
JOURNAL Submitted (10-APR-1999) Lineberger Comprehensive Cancer Center,
University of North Carolina at Chapel Hill, Mason Farm Rd. and
Manning Dr., Chapel Hill, NC 27599-7295, USA

FEATURES **Location/Qualifiers**
source 1..327
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
gene 1..327
 /gene="ROC1"
CDS 1..327
 /gene="ROC1"
 /note="Cullin partnering protein with associated ubiquitin
 ligase activity"
 /codon_start=1
 /product="RING finger protein"
 /protein_id="AAD30146.1"
 /db_xref="GI:4809216"
 /translation="MAAAMDVDTPSGTNSTGAGKKRFEVKKWNAAVALWAWDIVVDNCAI
 CRNHIMDLCIECQANQASATSEECTVAWGVCNHAHFHFCISRWLKTRQVCPLDNREWE
 FQKYGH"

BASE COUNT 85 a 75 c 94 g 73 t
ORIGIN

Alignment Scores:

Pred. No.:	5.64e-59	Length:	327
Score:	616.00	Matches:	108
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-541-462B-2 (1-108) x AF142059 (1-327)

Qy	1 Met Ala Ala Ala Met Asp Val Asp Thr Pro Ser Gly Thr Asn Ser Gly Ala Gly Lys Lys 20
Db	1 ATGGCGGCCAGCGATGGATGTGGATAACCCCGAGCGGCACCAAACAGCGCGCGGGCAAGAACAG 60
Qy	21 Arg Phe Glu Val Lys Lys Trp Asn Ala Val Ala Leu Trp Ala Trp Asp Ile Val Val Asp 40
Db	61 CGCTTTGAAGTGAAAAAGTGGATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT 120
Qy	41 Asn Cys Ala Ile Cys Arg Asn His Ile Met Asp Leu Cys Ile Glu Cys Gln Ala Asn Gln 60
Db	121 AACTGTGCCATCTGCAGGAACCACATTATGGATTTGCATAGAATGTCAAGCTAACCAAG 180
Qy	61 Ala Ser Ala Thr Ser Glu Glu Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe His 80
Db	181 GCGTCCCGTACTTCAGAAGAGTGTACTGTGCATGGGAGTCTGTAAACCAGCTTTCAC 240
Qy	81 Phe His Cys Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Arg Glu 100
Db	241 TTCCACTGCATCTCGCTGGCTAAACACGACAGGTGTGCCATTGGACAACAGAGAG 300
Qy	101 Trp Glu Phe Gln Lys Tyr Gly His 108
Db	301 TGGGAATTCCAAAAGTATGGGCAC 324

RESULT 2

AF140599

LOCUS AF140599 **504 bp** **mRNA** **linear** **ROD 11-MAY-1999**

DEFINITION Mus musculus ring-box protein 1 (Rbx1) mRNA, complete cds.
 ACCESSION AF140599
 VERSION AF140599.1 GI:4769005
 KEYWORDS
 SOURCE Mus musculus.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 504)
 AUTHORS Kamura,T., Koepp,D.M., Conrad,M.N., Skowyra,D., Moreland,R.J.,
 Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Elledge,S.J.,
 Conaway,R.C., Harper,J.W. and Conaway,J.W.
 TITLE Rbx1, a component of the VHL tumor suppressor complex and SCF
 ubiquitin ligase
 JOURNAL Science 284 (5414), 657-661 (1999)
 MEDLINE 99234320
 PUBMED 10213691
 REFERENCE 2 (bases 1 to 504)
 AUTHORS Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma
 Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA
 FEATURES Location/Qualifiers
 source 1..504
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 gene 1..504
 /gene="Rbx1"
 CDS 18..344
 /gene="Rbx1"
 /note="component of VHL tumor suppressor complex and SCF
 ubiquitin ligase"
 /codon_start=1
 /product="ring-box protein 1"
 /protein_id="AAD29716.1"
 /db_xref="GI:4769006"
 /translation="MAAAMDVDTPSGTNSGAGKKRFEVKKNATALWAHDIVVDNCAI
 CRNHIMDLCIECQANQASATSEECTVAWGVCNHAFFHCISRWLKTRQVCPLDNREWE
 FQKYGH"

BASE COUNT	117	a	107	c	137	g	143	t
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ORIGIN

Alignment Scores:

Pred. No.:	8.92e-59	Length:	504
Score:	616.00	Matches:	108
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-541-462B-2 (1-108) x AF140599 (1-504)

Qy	1 Met Ala Ala Ala Met Asp Val Asp Thr Pro Ser Gly Thr Asn Ser Gly Ala Gly Lys Lys 20
Db	18 ATGGCGGCCGGATGGATGTGGATAACCCCAAGGGCACCAACAGCGCCGGCAAGAAAG 77
Qy	21 Arg Phe Glu Val Lys Lys Trp Asn Ala Val Ala Leu Trp Ala Trp Asp Ile Val Val Asp 40

Db 78 CGCTTTGAAGTTAAAAGTGGAAATGCAGTGGCCCTCTGGGCTGGGACATTGTGGTTGAT 137
 Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 Db 138 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTGATCGAATGTCAGGCCAACCAG 197
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 198 GCGTCAGCTACTTCCGAAGAGTGTACGGTTGCATGGGAGTCTGCAACCATGCTTTCAT 257
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 Db 258 TTCCACTGCGATCTCTCGATGGCTCAAACGAGGCAGGTGTCCGGTGGACAACAGAGAG 317
 Qy 101 TrpGluPheGlnLysTyrGlyHis 108
 Db 318 TGGGAGTTCCAGAAGTATGGGCAT 341

RESULT 3

AF140598

LOCUS AF140598 508 bp mRNA linear PRI 11-MAY-1999
DEFINITION Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.
ACCESSION AF140598
VERSION AF140598.1 GI:4769003
KEYWORDS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS Kamura,T., Koepp,D.M., Conrad,M.N., Skowyra,D., Moreland,R.J.,
Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Elledge,S.J.,
Conaway,R.C., Harper,J.W. and Conaway,J.W.
TITLE Rbx1, a component of the VHL tumor suppressor complex and SCF
ubiquitin ligase
JOURNAL Science 284 (5414), 657-661 (1999)
MEDLINE 99234320
PUBMED 10213691
REFERENCE 2 (bases 1 to 508)
AUTHORS Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma
Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA
FEATURES Location/Qualifiers
source 1. .508
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1. .508
/gene="RBX1"
CDS 7. .333
/gene="RBX1"
/note="ring finger-like protein; component of VHL tumor
suppressor complex and SCF ubiquitin ligase"
/codon_start=1
/product="ring-box protein 1"
/protein_id="AAD29715.1"

/db_xref="GI:4769004"
/translation="MAAAMDVDPSTGNTSGAGKKRFEVKKNAVALWAUDIVVDNCAI
CRNHIMDLCIECQANQASATSEEECTVAWGVCNHFHFCISRWLKTRQVCPLDNREWE
FQKYGH"

BASE COUNT 126 a 106 c 124 g 152 t
ORIGIN

Alignment Scores:

Pred. No.:	8.99e-59	Length:	508
Score:	616.00	Matches:	108
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-541-462B-2 (1-108) x AF140598 (1-508)

Qy	1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20
Db	7 ATGGCGGCAGCGATGGATGTGGATAACCCGAGCGCACCAACAGCGCGCGGGCAAGAAAG	66
Qy	21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp	40
Db	67 CGCTTTGAAGTGAAAAGTGGAAATGCAGTAGCCCTCTGGCCTGGGATATTGTGGTTGAT	126
Qy	41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln	60
Db	127 AACTGTGCCATCTGCAGGAACACATTATGGATCTTGCATAGAATGTCAAGCTAACCAAG	186
Qy	61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80
Db	187 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGATGGGAGTCTGTAACCATGCTTTCAC	246
Qy	81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
Db	247 TTCCACTGCGATCTCTCGCTGGCTAAACACAGCAGGGTGTCCATTGGACAACAGAGAG	306
Qy	101 TrpGluPheGlnLysTyrGlyHis	108
Db	307 TGGGAATTCCAAAAGTATGGGCAC	330

RESULT 4

BC001466

LOCUS BC001466 544 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, ring-box 1, clone MGC:1481 IMAGE:3138751, mRNA,
complete cds.
ACCESSION BC001466
VERSION BC001466.1 GI:12655214
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 544)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2000) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 4 Row: j Column: 15.

FEATURES	Location/Qualifiers
source	1. .544 <i>/organism="Homo sapiens"</i> <i>/db_xref="LocusID:9978"</i> <i>/db_xref="taxon:9606"</i> <i>/clone="MGC:1481 IMAGE:3138751"</i> <i>/tissue_type="Placenta, choriocarcinoma"</i> <i>/clone_lib="NIH_MGC_21"</i> <i>/lab_host="DH10B-R"</i> <i>/note="Vector: pOTB7"</i>
CDS	15. .341 <i>/codon_start=1</i> <i>/product="ring-box 1"</i> <i>/protein_id="AAH01466.1"</i> <i>/db_xref="GI:12655215"</i> <i>/translation="MAAAMDVDTPSGTNSGAGKRFEVKKWNATALWAHDIVVDNCAI</i> <i>CRNHIMDLCIECQANQASATSEECTVAWGVNCNHAHFHFCISRWLKTRQVCPLDNREWE</i> <i>FQKYGH"</i>
BASE COUNT	157 a 107 c 129 g 151 t
ORIGIN	

Alignment Scores:
 Pred. No.: 9.67e-59 Length: 544
 Score: 616.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x BC001466 (1-544)

Qy 1 Met Ala Ala Ala Met Asp Val Asp Thr Pro Ser Gly Thr Asn Ser Gly Ala Gly Lys Lys 20

Db 15 ATGGCGGCAGCGATGGATGGATACCCGAGCGCACCAACAGCGCGGGCAAGAAG 74
 Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
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 Db 75 CGCTTTGAAGTGAAAAACTGGAATGCAGTAGGCCCTCTGGGCCTGGGATATTGTGGTTGAT 134
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 Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 |||||
 Db 135 AACTGTGCCATCTGCAGGAACCACATTATGGATTTGCATAGAATGTCAAGCTAACAG 194
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 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
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 Db 195 GCGTCCCGCTACTTCAGAAAGAGTGTACTGTCGATGGGAGTCTGTAACCAGCTTTCAC 254
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 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 |||||
 Db 255 TTCCACTGCGATCTCTCGCTGGCTAAACACGACAGGTGTGCCATTGGACAACAGAGAG 314
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 Qy 101 TrpGluPheGlnLysTyrGlyHis 108
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 Db 315 TGGGAATTCCAAAAGTATGGGCAC 338

RESULT 5

BC017370

LOCUS BC017370 554 bp mRNA linear PRI 14-NOV-2001
DEFINITION Homo sapiens, ring-box 1, clone MGC:13357 IMAGE:4065797, mRNA,
 complete cds.
ACCESSION BC017370
VERSION BC017370.1 GI:16924201
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 554)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 19 Row: c Column: 17

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657507.

FEATURES Location/Qualifiers
source 1. .554
/organism="Homo sapiens"
/db_xref="LocusID:9978"
/db_xref="taxon:9606"
/clone="MGC:13357 IMAGE:4065797"
/tissue_type="Brain, glioblastoma"
/clone_lib="NIH_MGC_57"
/lab_host="DH10B"
/note="Vector: pDNR-LIB"
CDS 23. .349
/codon_start=1
/product="ring-box 1"
/protein_id="AAH17370.1"
/db_xref="GI:16924202"
/translation="MAAAMDVDTPSGTNSGAGKRFEVKKWNAVALWAVIDVNCAI
CRNHIMDLCIECQANQASATSEEECTVAWGVCNHFHFCISRWLKTRQVCPLDNREWE
FQKYGH"
BASE COUNT 157 a 107 c 133 g 157 t
ORIGIN

Alignment Scores:

Pred. No.:	9.86e-59	Length:	554
Score:	616.00	Matches:	108
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-541-462B-2 (1-108) x BC017370 (1-554)

Qy	1 Met Ala Ala Ala Met Asp Val Asp Thr Pro Ser Gly Thr Asn Ser Gly Ala Gly Lys Lys 20
Db	23 ATGGCGGCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGGCCGGCAAGAACAG 82
Qy	21 Arg Phe Glu Val Lys Lys Trp Asn Ala Val Ala Leu Trp Ala Trp Asp Ile Val Val Asp 40
Db	83 CGCTTTGAAGTGAAAAGTGGATAGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 142
Qy	41 Asn Cys Ala Ile Cys Arg Asn His Ile Met Asp Leu Cys Ile Glu Cys Gln Ala Asn Gln 60
Db	143 AACTGTGCCATCTGCAGGAACACATTATGGATCTTGCATAGAATGTCAAGCTAACAG 202
Qy	61 Ala Ser Ala Thr Ser Glu Glu Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe His 80
Db	203 GCGTCCGCTACTTCAGAACAGTGACTGTCGATGGGAGTCTGTAACCAGCTTTCAC 262
Qy	81 Phe His Cys Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Arg Glu 100
Db	263 TTCCCACTGCATCTCGCTGGCTAAACACAGCAGGGTGTGCCATTGGACAACAGAGAG 322
Qy	101 Trp Glu Phe Gln Lys Tyr Gly His 108
Db	323 TGGGAATTCCAAAAGTATGGGCAC 346

RESULT 6
BC027396

LOCUS BC027396 1616 bp mRNA linear ROD 07-AUG-2002

DEFINITION Mus musculus, ring-box 1, clone MGC:35907 IMAGE:4952242, mRNA, complete cds.

ACCESSION BC027396

VERSION BC027396.1 GI:20072075

KEYWORDS MGC.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1616)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 60 Row: 1 Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9790190.

FEATURES Location/Qualifiers

source 1..1616
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N"
/clone="MGC:35907 IMAGE:4952242"
/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

CDS 7..333
/codon_start=1
/product="ring-box 1"
/protein_id="AAH27396.1"
/db_xref="GI:20072076"
/db_xref="LocusID:9978"
/translation="MAAAMDVDTPSGTNSGAGKKRFEVKKWNALWAVIDVDNCAI

CRNHIMDLCIECQANQASATSEECTVAWGVCNHFHFCISRWLKTRQVCPLDNREWE
FQKYGH"

BASE COUNT 453 a 330 c 407 g 426 t
ORIGIN

Alignment Scores:

Pred. No.:	3.06e-58	Length:	1616
Score:	616.00	Matches:	108
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-541-462B-2 (1-108) x BC027396 (1-1616)

Qy	1 Met Ala Ala Ala Met Asp Val Asp Thr Pro Ser Gly Thr Asn Ser Gly Ala Gly Lys Lys 20
Db	7 ATGGCGGCCGCGATGGATGTGGATACCCCCAGCGGCACCAACAGCGGCGCGGGCAAGAAG 66
Qy	21 Arg Phe Glu Val Lys Lys Trp Asn Ala Val Ala Leu Trp Ala Trp Asp Ile Val Val Asp 40
Db	67 CGCTTTGAAGTTAAAAGTGGAAATGCAGTGGCCCTCTGGGCCTGGGACATTGTGGTTGAT 126
Qy	41 Asn Cys Ala Ile Cys Arg Asn His Ile Met Asp Leu Cys Ile Glu Cys Gln Ala Asn Gln 60
Db	127 AACTGTGCCATCTGCAGGAACCACATTATGGATTTGTATCGAATGTCAGGCCAACCAG 186
Qy	61 Ala Ser Ala Thr Ser Glu Glu Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe His 80
Db	187 GCGTCAGCTACTCCGAAGAGTGTACGGTTGCATGGGAGTCTGCAACCATGCTTTCAT 246
Qy	81 Phe His Cys Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Arg Glu 100
Db	247 TTCCACTGCATCTCTCGATGGCTAAACAGGAGGTGTCCGTTGGACAACAGAGAG 306
Qy	101 Trp Glu Phe Gln Lys Tyr Gly His 108
Db	307 TGGGAGTTCCAGAAGTATGGGCAT 330

RESULT 7

AY027936

LOCUS AY027936 1933 bp mRNA linear VRT 19-MAR-2002
DEFINITION Salmo salar hyperosmotic protein 21 mRNA, complete cds.
ACCESSION AY027936
VERSION AY027936.1 GI:19067883
KEYWORDS
SOURCE Salmo salar.
ORGANISM Salmo salar
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
REFERENCE 1 (bases 1 to 1933)
AUTHORS Pan, F., Zarate, J. and Bradley, T.M.
TITLE A homolog of the E3 ubiquitin ligase Rbx1 is induced during
hyperosmotic stress of salmon
JOURNAL Am. J. Physiol. Regul. Integr. Comp. Physiol. 282 (2002) In press
REFERENCE 2 (bases 1 to 1933)

AUTHORS Bradley,T.M. and Pan,F.
 TITLE Direct Submission
 JOURNAL Submitted (22-FEB-2001) Fisheries, Animal and Veterinary Science,
 University of Rhode Island, Bldg.14, East Farm, Route 108,
 Kingston, RI 02881, USA
 FEATURES Location/Qualifiers
 source 1. .1933
 /organism="Salmo salar"
 /db_xref="taxon:8030"
 /tissue_type="gill"
 CDS 1135. .1704
 /note="SHOP21; putative E3 ubiquitin ligase; similar to
 human and murine RBX1 protein"
 /codon_start=1
 /product="hyperosmotic protein 21"
 /protein_id="AAK29182.1"
 /db_xref="GI:19067884"
 /translation="MSEGVPSPVCPSGTLAQAHQSPhRLPMEGQAAQAGSTNVWCRL
 LKASADHLIHVALRILCNVMHSHIVHLVPPNSARAIVNMAAAMDVDTPSATNSGASKKR
 FEVKKKNAVALWANDIVVDNCAICRNHIMDLCIECQANQASATSEECTVAWGVCNHAF
 HFHCISRWLKTRQVCPLDNREWEFQKYGH"
 BASE COUNT 518 a 466 c 443 g 506 t
 ORIGIN

Alignment Scores:

Pred. No.:	7.7e-57	Length:	1933
Score:	604.00	Matches:	106
Percent Similarity:	98.15%	Conservative:	0
Best Local Similarity:	98.15%	Mismatches:	2
Query Match:	98.05%	Indels:	0
DB:	5	Gaps:	0

US-09-541-462B-2 (1-108) x AY027936 (1-1933)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1378 ATGGCGGCAGCGATGGATGTTGATAACCCCAAGCGCACGAATAGTGGAGCAAGCAAGAAA 1437

 Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1438 CGTTTGAAAGTGAAGAAGTGGAAATGCACTGGCACTTGGGACTGGGACATTGTGGTGGAC 1497

 Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1498 AACTGTGCCATCTGTAGGAATCACATTATGGATCTGCATAGACTGCCAGGCTAACCAG 1557

 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1558 GCCTCTGCCACATCAGAGGAGTCACCGTAGCCTGGGAGTCTGCAATCATGCATTCCAT 1617

 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1618 TTCCACTGTATCTCCCGTTGGTTGAAGACCAGGCAGGTGTGCCCCCTAGACAACAGGGAG 1677

 Qy 101 TrpGluPheGlnLysTyrGlyHis 108
 ||||||| ||||| ||||| |||||
 Db 1678 TGGGAGTTTCAGAAATATGGACAC 1701

RESULT 8
HUMYQ60A05
LOCUS HUMYQ60A05 497 bp mRNA linear PRI 29-AUG-1998
DEFINITION Homo sapiens full length insert cDNA clone YQ60A05.
ACCESSION AF085906
VERSION AF085906.1 GI:3483246
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 497)
AUTHORS Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
Marth,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B.,
Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behymer,K., Hillier,L.,
Wilson,R. and Waterston,R.
TITLE Full Clone Sequencing of the Longest Available Member from Each
Unigene Cluster
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 497)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
<http://genome.wustl.edu/gsc>
<mailto:est@watson.wustl.edu>

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

SIMILARITY INFORMATION:
similar to *Caenorhabditis elegans* protein Z70757 (PID:g1262999)
ZK287.5

The location of this clone is unknown.

FEATURES Location/Qualifiers
source 1..497
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:200144"

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        /clone_lib="Soares_fetal_liver_spleen_1NFLS"
misc_feature    3. .305
                /note="similar to Caenorhabditis elegans protein Z70757
                        (PID:g1262999)"
misc_feature    18. .284
                /note="similar to Caenorhabditis elegans protein U80449
                        (PID:g1707068)"
misc_feature    36. .302
                /note="similar to Saccharomyces cerevisiae protein S66830
                        (PID:g2132017)"
misc_feature    42. .302
                /note="similar to Schizosaccharomyces pombe protein Z98977
                        (PID:g2388937)"
misc_feature    51. .284
                /note="similar to Caenorhabditis elegans protein Z46242
                        (PID:g559430)"

BASE COUNT      131 a      101 c      117 g      148 t
ORIGIN
```

Alignment Scores:

Pred. No.:	2.87E-55	Length:	497
Score:	584.00	Matches:	101
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	94.81%	Indels:	0
DB:	9	Gaps:	0

US-09-541-462B-2 (1-108) x HUMYQ60A05 (1-497)

Qy 8 AspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrp 27
 ||||| ||||| ||||| ||||| |||||
 Pb 3 GATACTCCCCCAACCCCCCGATGAGACGCCCCCGACGGATCCCTTTTGTCTGAGAGCTGG 62

Qy 28 AsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsn 47
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 AATGCGTAGCCCTCTGGGCTGGATATTGTGGTTGATAACTGTGCCATCTGCAGGAAC 122

Qy 48 HisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGlu 67
 |||||
 Db 123 CACATTATGCCATCTTTCGCAATAGCAATCTGCACCTAACGACCCCTCCGGTACTTGCAGAGCG 182

Qy 68 CysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrp 87
||||| ||||| ||||| ||||| |||||

Qy 88 LeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107

Qy 108 His 108

Db 303 CAC 305

RESULT 9
AY381680

AK281890/C
LOCUS

ACCESSION NUMBER AA261890 LENGTH 5347 bp DNA LINEAR PAI 02-NOV-2001
DEFINITION Sequence 99 from Patent WO0177389.

ACCESSION AX281690
 VERSION AX281690.1 GI:16608941
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,
 Mikita,T. and Tai,J.
 TITLE Genes expressed in foam cell differentiation
 JOURNAL Patent: WO 0177389-A 99 18-OCT-2001;
 Incyte Genomics, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..5347
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /note="Incyte ID No: 364940.19"
 BASE COUNT 1489 a 1277 c 1094 g 1487 t
 ORIGIN

Alignment Scores:

Pred. No.:	5.74e-53	Length:	5347
Score:	573.00	Matches:	103
Percent Similarity:	99.04%	Conservative:	0
Best Local Similarity:	99.04%	Mismatches:	0
Query Match:	93.02%	Indels:	1
DB:	6	Gaps:	0

US-09-541-462B-2 (1-108) x AX281690 (1-5347)

Qy	3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAla-GlyLysLysArgPh	22
Db	515 GCAGCGATGGATGTGGATACCCCGAGCGGCACCAAACAGCGCGCGGGCAAGAACGCGCTT	456
Qy	22 eGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCy	42
Db	455 TGAAGTAAAAAGTGGATGCAGTAGCCCTCTGGCCTGGATATTGTGGTTGATAACTG	396
Qy	42 sAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSe	62
Db	395 TGCCATCTGCAGGAACCACATTATGGATCTTGCATAGAATGTCAAGCTAACCGAGCGTC	336
Qy	62 rAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHi	82
Db	335 CGCTACTTCAGAAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTCACTCCA	276
Qy	82 scysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGl	102
Db	275 CTGCATCTCGCTGGCTAAAACACGACAGGTGTGCCATTGGACAACAGAGAGTGGGA	216
Qy	102 uPheGlnLys 105	
Db	215 ATTCCAAAAG 206	

RESULT 10
 HTEST/c

LOCUS HTEST 3484 bp mRNA linear PRI 01-MAY-1995
 DEFINITION H.sapiens mRNA for testican.
 ACCESSION X73608
 VERSION X73608.1 GI:793844
 KEYWORDS testican.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3484)
 AUTHORS Alliel,P.M., Perin,J.P., Jolles,P. and Bonnet,F.J.
 TITLE Testican, a multidomain testicular proteoglycan resembling
 modulators of cell social behaviour
 JOURNAL Eur. J. Biochem. 214 (1), 347-350 (1993)
 MEDLINE 93285162
 PUBMED 8389704
 FEATURES Location/Qualifiers
 source 1..3484
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="lambda gt11"
 CDS 435..1754
 /codon_start=1
 /product="testican"
 /protein_id="CAA51999.1"
 /db_xref="GI:793845"
 /db_xref="SPTREMBL:Q08629"
 /translation="MPAIAVLAAAAAAWCFLQVESRHL DALAGGAGPNHGNFLNDQW
 LSTVSQYDRDKYWNFRDDYFRNWNPNKPDFQALDPSKDPCLVKCSPHKVCVTQDY
 QTALCVSRKHLLPRQKGNVAQKHWVGPSNLVKCKPCPVAQSAMVCGSDGHSYTSKCK
 LEFHACSTGKSLATLCDGPCPCLPPEPEPPKHKKAERSACTDKELRNLASRLKDWF GALH
 EDANPIRKPTSSNTAQGRFDTSLIPICKDSLGLWMFNKLDMNYDLLLLDPSEINAIYLDK
 YEPCIKPLFNSCDSFKDGKLSNNEWCYCFQKPGGLPCQNEMRRIQKLSKGSKLLGAFI
 PRCNEEGYYKATQCHGSTGQCWCVDKYGNELAGSRKQGAVSCEEQETSGDFGS GSV
 VLLDDLEYERELGPDKKEGKLRVHTRAVTEDDEDDDEDEVGYIW"
 BASE COUNT 894 a 910 c 808 g 872 t
 ORIGIN

Alignment Scores:

Pred. No.:	4.45e-51	Length:	3484
Score:	554.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	89.94%	Indels:	0
DB:	9	Gaps:	0

US-09-541-462B-2 (1-108) x HTEST (1-3484)

Qy	3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe 22
Db	296 GCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGGCAAGAACGCCTT 237
Qy	23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCys 42
Db	236 GAA GTGAAA AGTGGATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATAACTGT 177
Qy	43 AlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62

Db 176 |||||||GCCATCTGCAGGAACCACATTATGGATCTTGCATAGAACGTAAGCTAACCGAGCGTCC 117
 Qy 63 AlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHis 82
 Db 116 GCTACTTCAGAAGAGTGACTGTCGCATGGGGAGTCTGTAAACCATGCTTTCACTTCCAC 57
 Qy 83 CysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 Db 56 TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGCCATTGGACAACAGAGAG 3

RESULT 11

AY099360

LOCUS AY099360 306 bp mRNA linear PRI 13-MAY-2002
DEFINITION Homo sapiens ZYP protein mRNA, partial cds.
ACCESSION AY099360
VERSION AY099360.1 GI:20502054
KEYWORDS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 306)
AUTHORS Perin,J.-P., Seddiqi,N., Charbonnier,F., Goudou,D., Belkadi,L., Rieger,F. and Alliel,P.M.
TITLE Genomic organization and expression of the ubiquitin-proteasome complex-associated protein Rbx1/ROC1/Hrt1
JOURNAL Cell. Mol. Biol. (Noisy-le-grand) 45 (8), 1131-1137 (1999)
MEDLINE 20106778
PUBMED 10643962
REFERENCE 2 (bases 1 to 306)
AUTHORS Alliel,P.M., Seddiqi,N., Belkadi,L., Lecoeur,L. and Perin,J.P.
TITLE Direct Submission
JOURNAL Submitted (23-APR-2002) U488, INSERM, 80, rue du General Leclerc, Le Kremlin-Bicetre 94270, France
FEATURES
 source Location/Qualifiers
 . 1..306
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="zyp3"
 /sex="male"
 /tissue_type="whole brain"
 /dev_stage="26-week fetus"
 /notes="caucasian"
 CDS <1..290
 /note="similar to RBX1/ROC1/HRT1"
 /codon_start=3
 /product="ZYP protein"
 /protein_id="AAM21718.1"
 /db_xref="GI:20502055"
 /translation="NSGASKKRFEVKKWNAVALWAUDIVVDNCAICRNHIMDLCIECQ
 ANQASATSEECTVAWGVCNHAHFHCISRWLKTRQVCPLDNREWEFQKYGH"

BASE COUNT 84 a 70 c 80 g 72 t

ORIGIN

Alignment Scores:

Pred. No.: 3.29e-51 Length: 306

Score: 545.00 Matches: 94
Percent Similarity: 98.95% Conservative: 0
Best Local Similarity: 98.95% Mismatches: 1
Query Match: 88.47% Indels: 0
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x AY099360 (1-306)

Qy 14 AsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrp 33
||| ||||| ||||| ||||| ||||| |||||
Db 3 AACAGCGCGAGCAAGAGCCTTGAAAGTGAAGTGGAAATGCAGTAGCCCTCTGG 62

Qy 34 AlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCys 53
||| ||||| ||||| ||||| |||||
Db 63 GCCTGGGATATTGTGGTTGATAACTGTGCCATCTGCAGGAACCACATTATGGATCTTG 122

Qy 54 IleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73
||| ||||| ||||| ||||| |||||
Db 123 ATAGAATGTCAAGCTAACAGCGTCGCTACTTCAGAAGAGTGTACTGTCGATGGGA 182

Qy 74 ValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93
||| ||||| ||||| ||||| |||||
Db 183 GTCTGTAACCATGCTTTCACTTCCACTGCATCTCGCTGGCTAAACACGACAGGTG 242

Qy 94 CysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
||| ||||| ||||| |||||
Db 243 TGTCCATTGGACAACAGAGAGTGGATTCAAAGTATGGGCAC 287

RESULT 12

AY119265

LOCUS AY119265 1181 bp mRNA linear INV 16-JUN-2002
DEFINITION Drosophila melanogaster SD23839 full insert cDNA.
ACCESSION AY119265
VERSION AY119265.1 GI:21430893
KEYWORDS FLI_CDNA.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydrioidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1181)
AUTHORS Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,
Champe,M., Chavez,C., Dorsett,V., Dresnek,D., Farfan,D., Frise,E.,
George,R., Gonzalez,M., Guarin,H., Kronmiller,B., Li,P., Liao,G.,
Miranda,A., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
Patel,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Rubin,G.M.
and Celtniker,S.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
COMMENT Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,

Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location in relation to other sequences, please visit our Web site (<http://fruitfly.berkeley.edu>) or send email to cdna@fruitfly.berkeley.edu.

FEATURES	Location/Qualifiers
source	1. .1181 /organism="Drosophila melanogaster" /db_xref="taxon:7227"
gene	1. .1181 /gene="Roc1a" /db_xref="FLYBASE:FBgn0025638"
CDS	162. .488 /gene="Roc1a" /note="Longest ORF" /codon_start=1 /product="SD23839p" /protein_id="AAM51125.1" /db_xref="GI:21430894" /db_xref="FLYBASE:FBgn0025638" /translation="MEVDEDGYEVPPSSSKGDKKRFEVKWNAVALWA DIVVDNCAI CRNHIMDLCIECQANQASATSEECTVAWGVCNHAFFHCISRLKTRQVCPLDNREWD FQKYGH"

BASE COUNT 346 a 246 c 288 g 301 t
ORIGIN

Alignment Scores:

Pred. No.:	1.73e-49	Length:	1181
Score:	535.00	Matches:	95
Percent Similarity:	90.09%	Conservative:	5
Best Local Similarity:	85.59%	Mismatches:	5
Query Match:	86.85%	Indels:	6
DB:	3	Gaps:	2

US-09-541-462B-2 (1-108) x AY119265 (1-1181)

QY 18 GlyLysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIle 37

QY 38 ValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGln 57

DB 273 GTGGTGGACAACCTGCGCCATCTGCGCGAACCATCATGGACTTGTCATCGAGTGTAG 332

Db 333 ||||||| GCGAACCAAGCGTCCGCCACTAGCGAGGTGCACCGTGGCCTGGGCGTCTGCAACCAC 392
 Qy 78 AlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAsp 97
 |||||||
 Db 393 GCCTTCCATTCCACTGCATCTCTCCCTGGCTAAAGACGCCAGGTATGCCACTGGAC 452
 |||||||
 Qy 98 AsnArgGluTrpGluPheGlnLysTyrGlyHis 108
 |||||:|||||:
 Db 453 AACCGCGAGTGGGATTCCAGAAGTACGGCCAC 485

RESULT 13

AY086913

LOCUS AY086913 635 bp mRNA linear PLN 26-JUN-2002
 DEFINITION Arabidopsis thaliana clone 29408 mRNA, complete sequence.
 ACCESSION AY086913
 VERSION AY086913.1 GI:21405628
 KEYWORDS FLI_CDNA.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 635)
 AUTHORS Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
 Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
 TITLE Full-length messenger RNA sequences greatly improve genome
 annotation
 JOURNAL Genome Biol. (2002) In press
 REFERENCE 2 (bases 1 to 635)
 AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
 Feldmann,K.
 TITLE Full-Length cDNA from Arabidopsis thaliana
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 635)
 AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
 Feldmann,K.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
 Malibu, CA 90265, USA
 COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made
 available to TIGR and Genbank. The following quality assessment of
 this set was done by comparison with known proteins: two percent of
 the clones are estimated to be 5'-truncated; less than one percent
 are 3'-truncated; approximately two percent represent alternative
 splice variants, including unspliced introns and spliced exons; one
 percent may contain premature stop codons; five percent may have
 frame shifts in a coding region. A sequence is considered to be
 5'-truncated if it lacks the translation initiation start (ATG). A
 sequence is considered to be 3'-truncated if it lacks the
 C-terminal end of the encoded protein. Please note that these cDNA
 sequences are derived from the Ws or LAer ecotypes and therefore
 may contain polymorphisms when compared to sequences from Col-0.
 Genset carried out the library production and sequencing of the
 full-length clones. Ceres, Inc. carried out the clustering of the
 5' sequences, selection of clones, and sequence assembly.
 FEATURES Location/Qualifiers

source 1. .635
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="29408"
CDS 91. .447
/codon_start=1
/product="ring-box protein-like"
/protein_id="AAM64477.1"
/db_xref="GI:21592528"
/translation="MATLDSDVTMIPAGEASSSVAASSSNKKAKRFEIKKWSAVALWA
WDIVVDNCAICRNHIMDLCIECQANQASATSEEECTVAWGVCNHAFFHCISRWLKTRQ
VCPLDNSEWEFQKYGH"

BASE COUNT 164 a 135 c 144 g 192 t

ORIGIN

Alignment Scores:

Pred. No.:	1.24e-47	Length:	635
Score:	515.50	Matches:	92
Percent Similarity:	83.19%	Conservative:	7
Best Local Similarity:	77.31%	Mismatches:	9
Query Match:	83.69%	Indels:	11
DB:	8	Gaps:	2

US-09-541-462B-2 (1-108) x AY086913 (1-635)

Qy	1 MetAlaAlaAlaMetAspValAspThr-----ProSerGly----- 12
	::: :::: : :
Db	88 TTAATGGCGACTCTAGACTCCGACGTTACCATGATTCCCTGCCGAGAACCTCCAGCAGC 147
Qy	13 -----ThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAla 29
	:::::: : : : : :
Db	148 GTAGCCGCCTCGTCTTCCAACAAGAAAGCTAACGATTGCAACTTAAGAAGTGGAGCGCC 207
Qy	30 ValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIle 49
	: : : : : : : : : : :
Db	208 GTTGCTCTCTGGGCTTGGGATATCGTTGACAACGTGCGATCTGCAGAAACCACATC 267
Qy	50 MetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThr 69
	: : : : : : : : : :
Db	268 ATGGATCTTGTATCGAGTGTCAAGGCTAACGCCCAGTGCCACAAGTGAAGAGTGCAC 327
Qy	70 ValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLys 89
	: : : : : : : : : :
Db	328 GTAGCTTGGGGGTTTCAATCACGCCCTCCACTTCAGTCATCAGCAGATGGCTAAAG 387
Qy	90 ThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
	: : : : : : : : :
Db	388 ACTCGTCAAGTTGTCATTGGATAACAGTGAGTGGAGTTCAAGAAATATGGTCAC 444

RESULT 14

AY072430

LOCUS	AY072430	666 bp	mRNA	linear	PLN 21-JAN-2002
DEFINITION	Arabidopsis thaliana ring-box protein - like (At5g20570) mRNA, complete cds.				
ACCESSION	AY072430				
VERSION	AY072430.1	GI:18252990			
KEYWORDS	FLI_CDNA.				

SOURCE *Arabidopsis thaliana*.
 ORGANISM *Arabidopsis thaliana*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; *Arabidopsis*.
 REFERENCE 1 (bases 1 to 666)
 AUTHORS Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
 Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
 Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
 Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
 Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
 Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (02-JAN-2002) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 COMMENT e-mail for correspondence: arab@sequence.stanford.edu

 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
*Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.

 The Salk, Stanford, PGEC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
 Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
 Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
 Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
 Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

 Nguyen,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
 equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
 (SSP/Stanford) contributed equally to this work as PIs.

 FEATURES Location/Qualifiers
 source 1. .666
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /chromosome="5"
 /clone="RAFL09-78-L12"
 /note="This clone is in pBluescript
 ecotype: Columbia"
 gene 1. .666
 /gene="At5g20570"
 CDS 88. .444
 /gene="At5g20570"
 /codon_start=1
 /product="ring-box protein - like"
 /protein_id="AAL62422.1"
 /db_xref="GI:18252991"
 /translation="MATLDSDVTMIPAGEASSSVAASSSNKKAKRFEIKKWSAVALWA
 WDIVVDNCAICRNHIMDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTQ
 VCPLDNSEWEFQKYGH"
 BASE COUNT 181 a 137 c 149 g 199 t
 ORIGIN*

Alignment Scores:

Pred. No.: 1.3e-47 Length: 666
 Score: 515.50 Matches: 92
 Percent Similarity: 83.19% Conservative: 7
 Best Local Similarity: 77.31% Mismatches: 9
 Query Match: 83.69% Indels: 11
 DB: 8 Gaps: 2

US-09-541-462B-2 (1-108) x AY072430 (1-666)

Qy	1 MetAlaAlaAlaMetAspValAspThr-----ProSerGly----- 12
	::: :: : :
Db	85 TTAATGGCGACTCTAGACTCCGACGTACCATGATTCCCTGCCGAGAACCTCCAGCAGC 144
Qy	13 -----ThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAla 29
	: :: : : : : :
Db	145 GTAGCCGCGTCGTCTCCAACAAGAAAGCTAACGATTGCAAATTAGAAGTGGAGCGCC 204
Qy	30 ValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIle 49
	: : : : : : : :
Db	205 GTTGCTCTCTGGCTTGGATATCGTTGACAACGTGCGATCTGCAGAAACCACATC 264
Qy	50 MetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThr 69
	: : : : : : :
Db	265 ATGGATCTTGTATCGAGTGTCAAGCTAACGCTGCCAACAGTGAAGAGTCGACT 324
Qy	70 ValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLys 89
	: : : : : : : :
Db	325 GTAGCTTGGGGGTTTCAATCACGCCCTTCAACTTCAGTCATCAGCAGATGGCTAAAG 384
Qy	90 ThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
	: : : : : : : :
Db	385 ACTCGTCAAGTTGTCCATTGGATAACAGTGAGTGGAGTTTCAGAAATATGGTCAC 441

RESULT 15

AY052401

LOCUS AY052401 357 bp mRNA linear PLN 16-OCT-2001
DEFINITION *Arabidopsis thaliana* ring box-1-like protein mRNA, complete cds.
ACCESSION AY052401
VERSION AY052401.1 GI:16186264
KEYWORDS
SOURCE *Arabidopsis thaliana*.
ORGANISM *Arabidopsis thaliana*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicots; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; *Arabidopsis*.
REFERENCE 1 (bases 1 to 357)
AUTHORS Okress, L.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-2001) Institute of Plant Biology, Biological
Research Center, Temesvari krt. 62, Szeged H-6701, Hungary
FEATURES Location/Qualifiers
source 1..357
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
CDS 1..357
/note="RBX1-2"
/codon_start=1

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/product="ring box-1-like protein"
/protein_id="AAL13435.1"
/db_xref="GI:16186265"
/translation="MATLSDVTMIPAGEASSVAAASSNNKAKRFEIKKWSAVALWA
WDIVDVNCACRNHIMDLCIECQANQASATSEECTVAWGVCNHAFFHCISRWLKTRQ
VCPLDNSEWEFQKYGH"
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BASE COUNT 91 a 83 c 94 g 89 t
ORIGIN

Alignment Scores:

Pred. No.: 8.67e-48 Length: 357
 Score: 514.50 Matches: 92
 Percent Similarity: 83.76% Conservative: 6
 Best Local Similarity: 78.63% Mismatches: 8
 Query Match: 83.52% Indels: 11
 DB: 8 Gaps: 2

US-09-541-462B-2 (1-108) x AY052401 (1-357)

Qy	3	AlaAlaMetAspValAspThr-----ProSerGly-----	12
	:::		:
Db	4	GCGACTCTAGACTCCGACGTTACCATGATTCTGCCGGAGAACGCTCCAGCAGCGTAGCC	63
Qy	13	---ThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaValAla	31
:::::	: : : : : : : : : : :		
Db	64	GCGTCGTCTTCCAACAAGAAAGCTAACCGATTGCAAATTAAGAAGTGGAGCGCCGTTGCT	123
Qy	32	LeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAsp	51
Db	124	CTCTGGGCTTGGGATATCGTTGACAACTGTGCGATCTGCAGAAACCACATCATGGAT	183
Qy	52	LeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAla	71
Db	184	CTTTGTATCGAGTGTCAAGCTAACAGGCCAGTGCCACAAGTGAAGAGTGCAGTGTAGCT	243
Qy	72	TrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArg	91
Db	244	TGGGGGGTTTGCATCACGCCCTCCACTTCACTGCATCAGCAGATGGCTAAAGACTCGT	303
Qy	92	GlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis	108
Db	304	CAAGTTTGTCCATTGGATAACAGTGAAGTGGGAGTTCAAGAAATATGGTCAC	354

Search completed: April 4, 2003, 17:52:09
Job time : 1471 secs

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame plus p2n model

Run on: April 4, 2003, 16:34:12 ; Search time 219 Seconds
(without alignments)
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